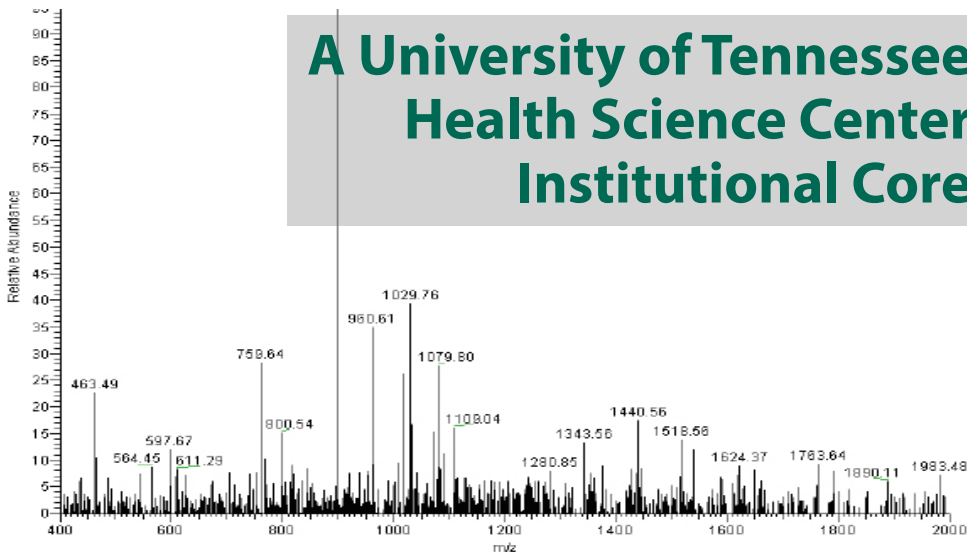


Proteomics and Metabolomics (PMC)



The PMC Core's mission is to provide the UTHSC community with state-of-the-art mass spectral technology and support to facilitate molecular-level discoveries that transform and advance our understanding of biological systems to solve challenging, relevant scientific questions in the life sciences.

Introduction & Services

The Proteomics and Metabolomics Core (PMC) was established through the Office of the Vice Chancellor for Research in 2015. The Core was created to provide resources for the highest quality mass spectrometry-based analysis supporting research needs in the fields of proteomics and metabolomics. The Core provides consultations to optimize experiment design and to interpret generated data. Services include identification and absolute or differential quantification of metabolites, drugs, and other small molecules in body fluids, cell and tissue extracts, identification of individual proteins in simple and highly complex protein mixtures, identification and mapping of posttranslational and other modifications of proteins, differential protein expression analysis based on precursor ion quantification (SILAC, dimethyl labelling), reporter ion quantification (iTRAQ/TMT labelling), and precursor ion area detection (label-free analysis), analysis of protein-protein interactions, and determination of the molecular masses of analytes.

Equipment and Software

The Core is equipped with a Thermo Orbitrap Fusion Lumos mass spectrometer - a tribrid mass spectrometer combining a Quadrupole, a Dual Linear Ion Trap, and an Orbitrap mass analyzers able to perform CID, HCD, ETD, ETcID, or EThcD fragmentation, operate in parallel mode, and provide excellent resolution (500,000 FWHM @m/z 200), accuracy (1 ppm), sensitivity (quantification of 1 attomole at CV<15%), and high scan rate (20 Hz). The instrument operates in line with an ultra-HPLC system- Ultimate 3000RSLC Nano for nano-flow applications or Vanquish for micro-flow applications. The software tools for system operation/data acquisition and post-acquisition analysis of raw MS data include Xcalibur/SII 4.0, Proteome Discoverer 2.1, PMI-Preview 2.11, PMI-

Byonic 2.11, Compound Discoverer 2.0, Tracefinder 4.1, Lipidsearch 4.1, and others.

Core Director

David Kakhniashvili, PhD, is the director of the Proteomics and Metabolomics Core at UTHSC. He earned his MS in Chemistry at Tbilisi State University (Rep. Georgia) and Ph.D. in Biochemistry at the Institute of Protein Research of Russian Academy of Sciences. He completed Mass Spectrometry-Biotech courses at the Thermo Electron Institute of West Palm Beach, Florida. Dr. Kakhniashvili has multiple publications in the field of proteomics related to red blood cells and sickle cell disease. He joined the UTHSC team in 2015.



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